AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

1-11. (Canceled)

12. (currently amended) A method for conferring resistance or tolerance to more than one virus selected from the group consisting of a furovirus, potyvirus, tospovirus [[or]] and cucomovirus upon a plant cell comprising the step of: introducing into a plant cell a first DNA sequence encoding a sense RNA fragment of a furovirus, potyvirus, tospovirus or cucomovirus genome or portion thereof and a second DNA sequence encoding an antisense RNA fragment of said furovirus, potyvirus or cucomovirus genome or portion thereof, wherein said sense RNA fragment and said antisense RNA fragment form a double-stranded RNA molecule when expressed in a plant cell, wherein the fragments of RNA are at least [[21]] 15 nucleotides in length and wherein the expression of said viral genomes or portions ~~genome or portion~~ thereof in said cell is reduced, and wherein said plant cell has resistance or tolerance to more than one virus selected from the group consisting of ~~said~~ furovirus, potyvirus, tospovirus [[or]] and cucomovirus.

13-15. (canceled)

16. (previously presented) The method of claim 12, wherein said DNA sequences comprises a nucleotide sequence obtained from a viral coat protein gene, a viral nucleocapsid protein gene, a viral replicase gene, a movement protein gene or portions thereof.

17. (original) The method of claim 12, wherein said first DNA sequence and said second DNA sequence are stably integrated in the genome of said cell.

18. (original) The method of claim 12, wherein said first DNA sequence and said second DNA sequence are comprised in two different DNA molecules.

19. (original) The method of claim 18, wherein said DNA molecules further comprise a first promoter operably linked to said first DNA sequence and a second promoter operably linked to said second DNA sequence.

20. (original) The method of claim 12, wherein said first DNA sequence and said second DNA sequence are comprised in one DNA molecule.

21. (original) The method of claim 20, wherein said first DNA sequence and said second DNA sequence are comprised in the same DNA strand of said DNA molecule.

22. (original) The method of claim 21, wherein said sense RNA fragment and said antisense RNA fragment are comprised in one RNA molecule.

23. (original) The method of claim 22, wherein said RNA molecule is capable of folding such that said RNA fragments comprised therein form a double-stranded region.

24. (original) The method of claim 22, wherein said DNA molecule further comprises a promoter operably linked to said first or said second DNA sequence.

25. (original) The method of claim 24, wherein said promoter is a heterologous promoter.

26. (original) The method of claim 24, wherein said promoter is a tissue-specific promoter.

27. (original) The method of claim 24, wherein said promoter is a developmentally regulated promoter.

28. (original) The method of claim 24, wherein said promoter is a constitutive promoter.

29. (original) The method of claim 24, wherein said promoter is an inducible promoter.

30. (original) The method of claim 22, wherein said DNA molecule further comprises a linker between the DNA sequences encoding said sense RNA fragment and said antisense RNA fragments.

31-33. (canceled)

34. (previously presented) The method of claim 30, wherein the linker comprises intron processing signals.

35. (original) The method of claim 21, wherein said sense RNA fragment and said antisense RNA fragment are comprised in two RNA molecules.

36. (original) The method of claim 35, wherein said first DNA sequence is operably linked to a first promoter and said second DNA sequence is operably linked to a second promoter.

37. (original) The method of claim 35, wherein said first DNA sequence and said second DNA sequence are operably linked to a bi-directional promoter.

38. (original) The method of claim 21, wherein said first DNA sequence and said second DNA sequence are comprised in complementary strands of said DNA molecule.

39. (original) The method of claim 38, wherein said first DNA sequence is the complementary DNA strand of said second DNA sequence in said DNA molecule.

40. (original) The method of claim 39, wherein said DNA molecule further comprises a first promoter operably linked to said first DNA sequence.

41-48. (canceled)

49. (currently amended) A plant comprising the plant cell of claim 76 [[47]], wherein the plant is virus resistant or tolerant to more than one virus selected from the group consisting of said furovirus, potyvirus, tospovirus [[or]] and cucomovirus.

50-55. (canceled)

56. (currently amended) A plant regenerated from the plant cell of claim 76 [[60]], wherein the plant is resistant or tolerant to more than one virus selected from the group consisting of said furovirus, potyvirus, tospovirus [[or]] and cucomovirus.

57. (canceled)

58. (currently amended) Seeds ~~regenerated~~ produced from the plant of claim 56, wherein said seeds are resistant or tolerant to more than one virus selected from the group consisting of said furovirus, potyvirus, topsovirus [[or]] and cucomovirus.

59-72. (canceled)

73. (previously presented) The plant cell of claim 76, wherein the expression of said viral genomes or portions ~~genome or portion~~ thereof in said cell [[is]] are reduced, and wherein said DNA sequences are expressed, and wherein said cell is resistant or tolerant to more than one virus selected from the group consisting of said furovirus, potyvirus, topsovirus, [[or]] and cucomovirus.

74-75. (canceled)

76. (currently amended) A plant cell obtained by the method of claim 12, wherein said cell is resistant or tolerant to more than one virus selected from the group consisting of said furovirus, potyvirus, topsovirus [[or]] and cucomovirus.

77. (previously presented) The method of claim 12, wherein said DNA sequences comprises a nucleotide sequence obtained from a furovirus replicase gene or portion thereof.

78. (previously presented) The method of claim 12, wherein said DNA sequences comprises a nucleotide sequence obtained from the beet necrotic yellow vein virus (BNYVV).

79. (previously presented) The method of claim 78, wherein said DNA sequences comprises a nucleotide sequence obtained from the replicase gene (RNA1) of the beet necrotic yellow vein virus or portion thereof.

80. (previously presented) The method of claim 79, wherein the portion of the replicase gene from BNYVV comprises the 3' end.

81. (currently amended) The method of claim 80, wherein the portion of the replicase gene from BNYVV is ~~about 450~~ 452 nucleotides.

82. (currently amended) The method of claim 81, wherein the portion of the replicase gene from BNYVV is from nucleotide 5168 to nucleotide 5620 of Genbank accession no. D00115.

83. (previously presented) The method of claim 12, wherein said DNA sequences comprises a nucleotide sequence obtained from a potyvirus or portion thereof.

84. (previously presented) The method of claim 12, wherein said DNA sequences comprises a nucleotide sequence obtained from a tospovirus or portion thereof.

85. (previously presented) The method of claim 12, wherein said DNA sequences comprises a nucleotide sequence obtained from a cucomovirus or portion thereof.

86. (currently amended) Progeny obtained from the plant of claim 56, wherein said progeny are resistant or tolerant to more than one virus selected from the group consisting of said furovirus, potyvirus, tospovirus [[or]] and cucomovirus.

87. (New) The method of claim 12, wherein the RNA fragment is at least 50 nucleotides in length.

88. (New ) The method of claim 12, wherein the RNA fragment is at least 150 nucleotides in length.

89. (New) The method of claim 12, wherein the RNA fragment is at least 500 nucleotides in length.